Deriving field-based species sensitivity distributions (f-SSDs) from stacked species distribution models (S-SDMs)

Aafke M. Schipper*, Leo Posthuma†, Dick de Zwart‡, Mark A.J. Huijbregts†

† Radboud University, Institute for Water and Wetland Research, Department of Environmental Science, PO Box 9010, 6500 GL Nijmegen, The Netherlands
‡ National Institute for Public Health and the Environment (RIVM), Centre for Sustainability, Environment and Health, PO Box 1, 3720 BA Bilthoven, The Netherlands
* A.Schipper@science.ru.nl

KEYWORDS
biodiversity, freshwater ecosystems, species distribution modelling (SDM), species richness, species sensitivity distribution (SSD), stressor-response relationships
ABSTRACT

Quantitative relationships between species richness and single environmental factors, also called species sensitivity distributions (SSDs), are helpful to understand and predict biodiversity patterns, identify environmental management options and set environmental quality standards. However, species richness is typically dependent on a variety of environmental factors, implying that it is not straightforward to quantify SSDs from field monitoring data. Here, we present a novel and flexible approach to solve this, based on the method of stacked species distribution modelling. First, a species distribution model (SDM) is established for each species, describing its probability of occurrence in relation to multiple environmental factors. Next, the predictions of the SDMs are stacked along the gradient of each environmental factor with the remaining environmental factors at fixed levels. By varying those fixed levels, our approach can be used to investigate how field-based SSDs for a given environmental factor change in relation to changing confounding influences, including for example optimal, typical or extreme environmental conditions. This provides an asset in the evaluation of potential management measures to reach good ecological status.
INTRODUCTION

Quantitative relationships between species richness and particular environmental factors are an asset to better understand biodiversity patterns, identify environmental management options and priorities, and set environmental quality standards.\textsuperscript{1-4} It is, however, not straightforward to reveal such relationships for single environmental factors, because species richness is typically dependent on a multitude of environmental factors.\textsuperscript{5} Laboratory settings offer an opportunity to study biotic responses to specific environmental factors by eliminating confounding environmental influences. This is typically done for toxic substances, in order to establish biotic response curves called species sensitivity distributions (SSDs), i.e., response curves that describe inter-species variation in sensitivity to a toxicant of concern by showing the expected proportion of species affected in relation to increasing levels of toxicant exposure.\textsuperscript{6} Yet, not all species and environmental factors lend themselves to laboratory testing, implying that such laboratory-based response curves are biased towards easily cultured species and a limited set of environmental factors. Species richness response curves derived from field monitoring data, also called field-based species sensitivity distributions (f-SSDs), are expected to be ecologically more relevant, as these cover the actual species pool and all relevant environmental factors of a particular area.\textsuperscript{7, 8}

Recently, various methods have been proposed to establish f-SSDs. Site-specific species richness observations can be directly related to a particular environmental factor with piece-wise regression or quantile regression.\textsuperscript{4, 9} With quantile regression based on one of the upper boundaries of the response variable distribution (e.g. the 0.95 or 0.99 quantile), the resulting response curves are expected to show the constraints imposed by the environmental factor of concern.\textsuperscript{4, 9} Two further methods assess the number of species within predefined intervals along a particular environmental gradient based on multiple samples pooled per interval. The number of
species per interval is then determined either by simply counting the number of unique species
across all samples within the interval, or by establishing a species accumulation curve (SAC)
per interval, in order to correct for potential differences in the number of samples among the
intervals. Alternative methods first relate species-specific abundance or occurrence to a
particular environmental factor, and then aggregate (‘stack’) the results across multiple species to
arrive at an f-SSD. Leung et al., for example, modelled the abundance of benthic
macroinvertebrate taxa in relation to sediment toxicant concentrations on the Norwegian
continental shelf and stacked the toxicant concentrations corresponding with 50% abundance
reductions. Presence-absence or presence-only data, which are generally more readily available
than abundance data, have been used to establish species-specific field-based occurrence
ranges, which were then stacked across the species.

Despite the differences in approach, however, the f-SSDs in the studies cited above were all
derived by relating the response variable (species richness or species-specific abundance or
occurrence) exclusively to the environmental factor of concern. In the present study, we present
an approach to derive f-SSDs that explicitly account for the confounding influences of other
environmental factors. Our method is based on stacked species distribution modelling (S-SDM),
where species richness for a site is calculated by adding up the predictions of single species
distribution models. We first establish a species distribution model (SDM) for each
individual species, describing its probability of occurrence in relation to multiple environmental
factors. These SDMs are used to predict and stack the probabilities of occurrence of all modelled
species in relation to each environmental factor by varying this factor across its range while
setting the other environmental factors at fixed levels. As these fixed levels can be varied, our
method provides a flexible approach to response curve modelling that can be used to investigate
the dependency of f-SSDs on changing confounding influences.

MATERIALS AND METHODS

Dataset
We used a monitoring dataset comprising 379 observations of benthic macroinvertebrate taxa
and co-occurring abiotic conditions. Samples were collected from 1992 to 2004 from various
tidally influenced freshwater bodies in the western part of The Netherlands (Figure 1).
Macroinvertebrate data comprised the presence-absence of in total 220 taxa. For our study, we
selected taxa that were observed in at least 10 samples. Of the 82 taxa with more than 10
observations, 53 were identified on species level, 22 on genus level and 7 on family level (Table
S1). Yet, we will further refer to species (and species richness) rather than taxa (and taxonomic
richness), in order to link up with the SDM and SSD terminology. Species richness ranged from
1 to 41 with an average of 15 across all samples (Table 1). Abiotic variables included (1)
Biesbosch area (binary variable indicating whether samples originated from the Biesbosch nature
reserve area (n=91) or not (n=288)), (2) shipping (binary variable indicating whether shipping
activities took place at the sampling site (n=150) or not (n=229)), (3) water depth (m), (4) tidal
amplitude (cm), (5) sedimentation rate (cm/yr), (6) sediment sand content (% dry wt; particle
size > 210 μm), (7) sediment clay content (% dry wt; particle size < 2 μm), (8) sediment dry
matter content (% wet wt), (9) sediment organic matter content (% dry wt), (10) sediment pH
(based on KCl-extraction), and (11) mixture toxic pressure (msPAFEC50). Assessing the
combined pressure of multiple toxicants is relatively uncommon in bioassessments, but has
become possible due to the mixture toxic pressure concept. Mixture toxic pressure was
quantified as the multi-substance potentially affected fraction of species (msPAF) due to 45 contaminants (eight metals, 16 chlorinated organics, mineral oil, 16 polycyclic aromatic hydrocarbons (PAHs), and four polychlorinated biphenyls (PCBs)). Mixture toxic pressure values were derived from the sample-specific concentrations of the contaminants combined with substance-specific toxicity data for various test species. Toxicity data pertained to toxicant concentrations resulting in 50% of the individuals being affected (EC50). More details regarding the monitoring data and the toxic pressure calculations can be found in Posthuma and De Zwart. The distributional characteristics of the continuous abiotic variables are provided in Table 1.

**Data processing**

We standardized all continuous abiotic variables to zero mean and unit variance. To account for potentially bell-shaped (unimodal) associations between species occurrence and environmental factors, we added the quadratic terms for all but the categorical abiotic variables, thus obtaining a set of 20 potential predictors to fit the SDMs. We tested for multicollinearity among the predictors by calculating variance inflation factors (VIFs) and removed predictors with a VIF > 5 one by one, until all remaining predictors had a VIF < 5. This resulted in the removal of three abiotic variables from the initial set, i.e., sediment dry matter content, sediment clay content and tidal amplitude (Table S2).

**Fitting the SDMs**

As our macroinvertebrate observations were binary (presence-absence), we constructed our SDMs using multiple logistic regression with a logit link and binomial error distribution. We fitted all possible combinations of predictors, whereby we allowed quadratic predictor terms only if the linear term was included as well, in order to obtain models insensitive to linear transformations of the predictors. The resulting models were ranked according to Akaike’s
Information Criterion (AIC), thus identifying the most parsimonious models amongst a set of models with comparable fit. Per species, we calculated weighted average regression coefficients based on the set of models within 2 AIC units from the ‘best’ model, i.e., the model with the lowest AIC (Text section S1). Model building and averaging was done with the package MuMIn in R. We evaluated the resulting SDMs for residual spatial autocorrelation, because considerable residual autocorrelation would point at inappropriate model specification (for example, only linear terms are specified whereas non-linear terms would be required), missing key environmental predictors, or significant biotic interactions. We quantified the residual spatial autocorrelation of each SDM as Moran’s I autocorrelation coefficient based on the deviance residuals, using the APE package in R. Next, we evaluated the accuracy of our SDMs based on the area under the curve (AUC) of the receiver-operating characteristics (ROC) plots. We selected AUC as a goodness-of-fit measure because AUC does not rely on an arbitrary threshold to classify predicted probabilities of occurrence into presence-absence values. We calculated AUC values not only for the fitted SDMs, but also in a cross-validation procedure. To cross-validate the SDMs, we randomly divided our dataset into a training and test set, containing 80% and 20% of the total cases, respectively. The training data set was used to generate SDMs, which were then used to make predictions for the observations in the test data set. We did this five times (5-fold cross-validation), thereby ensuring that each observation was included in a test set once. AUC-values were obtained with the R package PresenceAbsence.

Establishing the f-SSDs

To obtain the f-SSDs, we stacked the predictions of the SDMs, i.e., we summed the predicted probabilities of occurrence, according to:

\[ SR_{pred} = \sum_{n=1}^{n=i} P_i \]  

(Eq. 1)
where $SR_{pred}$ represents the predicted species richness and $p_i$ represents the probability of occurrence predicted for species $i$.\textsuperscript{13,14} We applied Eq. 1 to estimate species richness in relation to each of the abiotic variables separately while keeping the other abiotic variables at fixed levels. This enabled us to investigate how the biotic responses to a particular abiotic variable changed with changing levels of the other abiotic variables. We applied three sets of fixed levels, i.e., the median values of the observations, and the levels resulting in, respectively, the highest (‘optimum’) and lowest (‘worst case’) values of $SR_{pred}$ for our study area (Table 2), which we identified with the Solver tool of Microsoft Excel. We identified the optimum and worst case abiotic conditions for species richness rather than for single species, because a species-by-species evaluation would not result in a single set of optimum or worst case abiotic conditions. Further, we identified the optimum and worst case conditions for all abiotic variables simultaneously, because these values are not independent of each other. Finally, to ensure that the optimum and worst case values were representative for our study area, we restricted the levels of all abiotic variables to the ranges as measured across the observations (Table 1).

To evaluate the accuracy of our S-SDM, we assessed species richness based on the sample-specific abiotic conditions and compared these model estimates with the species richness observed. This was done based on the fitted as well as the cross-validated SDMs. We also confronted our S-SDM with a regression model relating species richness directly to the abiotic variables. This model, hereafter referred to as the macroecological model (MEM),\textsuperscript{13} was obtained by fitting a generalized linear model with a log link and a Poisson distribution. Similar to the SDMs, the MEM was obtained by fitting all possible combinations of predictors, allowing quadratic terms only together with linear terms, and calculating weighted average regression coefficients based on the set of models within 2 AIC units from the ‘best’ model. We also
evaluated the MEM according to a 5-fold cross-validation. Overall performance of the fitted and cross-validated S-SDMs and MEMs was calculated as

\[
R^2 = 1 - \frac{\sum_{i=1}^{n}(P_i - O_i)^2}{\sum_{i=1}^{n}(O_i - \bar{O})^2}
\]  
(Eq. 2)

where \(O_i\) and \(P_i\) refer to the species richness observed and predicted, respectively, for sample \(i\), and \(\bar{O}\) represents the overall mean of the species richness observed. This measure of \(R^2\) ranges from minus infinity to 1, with positive values indicating that the model estimates outperform the mean of the observed values, whereas negative values indicate that the mean of the observations is a better predictor.\(^{27}\)

**RESULTS**

**SDMs**

The residual spatial autocorrelation of the fitted SDMs was, on average, close to the expected value of -0.003 corresponding with the null hypothesis of no spatial autocorrelation (Table S3). The deviance explained by the fitted SDMs was on average 23\% and the AUC was on average 0.84 (Table S3). Of the 82 fitted models, 76 had an AUC value of > 0.7 and 25 had AUC > 0.9, indicating adequate and highly accurate model performance, respectively.\(^{23, 28}\) Cross-validated SDMs, however, had considerably lower AUC values than the fitted models. On average, the AUC showed a drop of 0.3 from the fitted to the cross-validated SDMs (Table S3).

The probabilities of occurrence as predicted by our models varied among the species and among the abiotic variables. As examples, we show the responses of the chironomid species *Einfeldia carbonaria*, the dreissenid species *Dreissena polymorpha* and the invasive gastropod...
species *Potamopyrgus antipodarum* to each of the eight abiotic variables (Figure 2). Responses to the continuous abiotic variables included monotonically increasing or decreasing probabilities of occurrence as well as unimodal and bimodal curves. Both the intercept and the shape of the response curves tended to change in response to changing confounding environmental influences. Under worst case confounding conditions, the three species generally showed little to no response to the abiotic variable of interest.

**Stacking the SDMs**

Both the fitted and the cross-validated S-SDM yielded estimates of species richness that clearly outperformed the mean of the observations ($R^2$ of 0.52 and 0.44, respectively). The S-SDM also outperformed the MEM, although the difference in performance was small in particular for the fitted models (Figure 3). Irrespective of the method used, species richness tended to be overestimated for species-poor samples and underestimated for species-rich samples (Figure 3).

**f-SSDs**

Similar to the three example species (Figure 2), species richness showed little response to particular abiotic variables if the other abiotic variables were set at worst case values (Figure 4). With the confounding variables optimized in terms of species richness, the f-SSDs tended to follow the highest species richness observed in the field, with few observations exceeding the predicted values. According to these response curves, the macroinvertebrate species richness in our study area varied mostly in relation to sedimentation rate, followed by water depth and mixture toxic pressure. A unimodal response of species richness was observed in relation to sedimentation rate, whereas a monotonic decrease was found for water depth. For mixture toxic pressure, the curve showed a slight increase in species richness followed by a clear decrease (Figure 4). The f-SSDs based on the MEM were mostly of similar shape as those based on the S-
SDMs (Figure S1), except for pH, where the MEM-based curve for optimum confounding conditions showed a monotonic decrease in species richness with increasing pH instead of a unimodal response.

DISCUSSION

Model performance

Stacked species distribution modelling (S-SDM), i.e., aggregating the predictions of multiple single species distribution models, constitutes a recent approach to obtain estimates of community-level properties like species richness. The approach is encouraged in particular by the increasing availability of large-scale, multispecies data sets and advances in modelling techniques and software. S-SDM has typically been applied to obtain site-specific species richness estimates. To our knowledge, we are the first to use S-SDM in order to construct f-SSDs. We tested our approach on a monitoring dataset of freshwater macroinvertebrates and co-occurring abiotic variables. Although our fitted SDMs performed adequately for the majority of the species (AUC > 0.7), the cross-validated SDMs were characterized by considerably lower AUC values (Table S3). A large drop in model performance from a fitted to a cross-validated model may point at overfitting: the model may be so well adapted to the training dataset that it performs poorly when applied to other circumstances. Although Akaike’s Information Criterion is supposed to correct for overfitting by including a penalty for each additional parameter, it has been suggested that the penalty is not large enough to effectively prevent overfitting. This indicates that it is worth to consider more stringent criteria for predictor inclusion, for example the Bayesian Information Criterion (BIC), if the SDMs are to be used for extrapolation beyond the training dataset. Despite the poor performance of the cross-validated
SDMs, however, the variation in species richness explained by the cross-validated stacked model was only 8 percentage points lower than the variation explained by the fitted S-SDM (Figure 3). Apparently, the uncertainties in the probabilities of occurrence predicted for single species largely cancelled out in the stacking procedure. The slight over- and underestimation of species richness for species-poor and species-rich samples, respectively, are in line with other studies where species richness was estimated by summing occurrence probabilities.\textsuperscript{13, 37} This pattern seems to result from the range of the SDM predictions being smaller than the range of the observations: the observational data consist exclusively of zeros and ones, whereas the modelled probabilities typically take values in between zero and one.

**Interpretation and application**

We obtained our f-SSDs by varying particular environmental factors across their ranges while keeping the other environmental factors at fixed levels. If these fixed levels are optimized towards maximum species richness, our f-SSDs can be interpreted like quantile regression curves based on one of the upper values of the response variable distribution.\textsuperscript{5, 9} Identification of the optimum environmental conditions revealed that macroinvertebrate species richness in our study system tends to be highest in the littoral zone (water depth $\approx 0$), and at a mixture toxic pressure value of 0.11 (Table 2). The latter may reflect hormesis: at low to moderate pollution levels, organisms may not just repair toxicant-induced damage, but also overcompensate with elevated vitality and fitness.\textsuperscript{38} Alternatively, low to moderate pollution levels may reduce organism abundance and competitive ability, thus leaving room for additional species to establish, as described by the intermediate disturbance hypothesis.\textsuperscript{39}

Our results further showed that a Poisson regression model directly based on species richness allows to obtain results similar to the S-SDM approach, i.e., response curves and corresponding
values of confounding environmental factors (Figure S1, Table S4). However, in contrast to regressing species richness directly on the explanatory variables, the S-SDM approach also quantifies the responses of individual species to particular environmental factors (Figure 2). As habitat preferences and environmental responses vary among species, conditions that are best or worst in terms of overall species richness are not necessarily best or worse for each single species. Given that conservation practitioners are often interested not only in mere species richness but also in the occurrence of single, focal species and in community composition\textsuperscript{13}, the S-SDM approach thus provides additional information relevant for targeted environmental management.

Apart from the present study, there are various other recent studies that quantified and aggregated the environmental responses of single species to derive f-SSDs. In these studies, species-specific occurrence data were linked to the environmental factor of concern either to derive the highest or nearly highest level of this factor where each species was observed, or to quantify species-specific field-based tolerance ranges, i.e., ranges between the minimum and maximum level of the environmental factor where the species was found.\textsuperscript{3, 12} Subsequently, these species-specific field-based occurrence thresholds or tolerance ranges were stacked to arrive at f-SSDs, whereby each species added to the total species richness as long as the environmental factor was below its occurrence threshold or within its tolerance range. Thus, f-SSDs directly derived from raw occurrence data do not account for inter-species variation in occurrence caused by factors other than the environmental factor of concern, but assess the number or proportion of species potentially occurring at a given level of a particular environmental factor, irrespective of confounding influences of other environmental factors.\textsuperscript{10} In contrast, our response curves rely on modelled probabilities of occurrence rather than raw presence-absence data and thus account for
the influences of multiple environmental factors on the occurrence probability of each species.

These include not only the other measured environmental factors (via the regression coefficients of the SDMs), but also unmeasured environmental influences (via the intercepts), which may include unmeasured abiotic variables as well as biotic interactions. Thus, our approach yields response curves that are conditional on the confounding effects of other factors, which implies that they can be used in site-specific assessments. For example, our approach can be used to translate measured abiotic conditions at a particular site to estimates of species composition and richness, similar to the RIVPACS approach. This provides an asset when alternative management scenarios are considered, for example when the aim is to achieve good ecological status according to the European Water Framework Directive.

SUPPORTING INFORMATION

The following material is available as supporting information to this paper:

Table S1: List of macroinvertebrate taxa included in this study.

Table S2: Variance inflation factors (VIFs) of the selected predictors.

Table S3: Species distribution models (SDMs) of the 82 macroinvertebrate taxa.

Text section S1: Equations used to calculate weighted average regression coefficients.

Table S4: Three sets of fixed environmental conditions used to obtain f-SSDs from the MEM.

Figure S1: f-SSDs derived from the MEM, showing macroinvertebrate species richness in relation to eight abiotic variables in tidally influenced freshwater bodies in The Netherlands.

This material is available free of charge via the Internet at http://pubs.acs.org.

ACKNOWLEDGEMENT
We thank L. Osté and J. Hin (Deltares) for initiating the analyses of this data set, many colleagues for collecting samples and providing the data, and E.T.H.M. Peeters (Wageningen University), H.J. de Lange (Alterra), M.A.A. de la Haye, H.A. Rutjes, L.M. Janmaat (Grontmij), B. Reeze (Arcadis), and J.F. Postma (EcoFide) for preliminary data analyses. Further, we thank Z.J.N. Steinmann (Radboud University Nijmegen) and I. Soenario (KNMI) for helping out with coding in R and Python, and L.B. Azevedo (Radboud University) for insightful discussions regarding f-SSD modelling. This research project was funded by the Director-General of the Dutch National Institute for Public Health and the Environment (RIVM) in the framework of the strategic research program as run under the auspices of RIVM’s Scientific Advisory Board, in the projects S/607001, S/607002 and S/607020, and by EU-FP7 ‘SOLUTIONS’ (grant agreement no: 603437).

REFERENCES


20. Bartoń, K. *MuMIn: Multi-model inference. R package 1.9.5*, [http://cran.r-project.org/web/packages/MuMIn/index.html](http://cran.r-project.org/web/packages/MuMIn/index.html); 2009.


Figure 1. Sampling locations of macroinvertebrates and abiotic conditions in tidally influenced freshwater bodies in the western part of The Netherlands.
Figure 2. The probability of occurrence ($p$) of *Einfeldia carbonaria* (left), *Dreissena polymorpha* (centre) and *Potamopyrgus antipodarum* (right) and in relation to eight abiotic variables in tidally influenced freshwater bodies in The Netherlands.
Figure 3. Observed versus predicted species richness for a) the fitted S-SDM, b) the fitted MEM, c) the cross-validated S-SDM and d) the cross-validated MEM. The dashed black lines indicate perfect model fit; the solid grey lines represent the relationship between predicted and observed species richness according to a least-squares linear regression. \( R^2 \) values were calculated according to Eq. 2.
Figure 4. f-SSDs derived from S-SDMs, showing macroinvertebrate species richness in relation to eight abiotic variables in tidally influenced freshwater bodies in The Netherlands. For the categorical abiotic variables (‘Biesbosch area’ and ‘shipping’), the observations are represented by the median and range.
Table 1. Means, standard deviations (SD), ranges (minimum, maximum) and quartiles of macroinvertebrate species richness and the nine continuous abiotic variables as measured across the observations (n=379).

<table>
<thead>
<tr>
<th>Variable (unit)</th>
<th>mean</th>
<th>SD</th>
<th>min</th>
<th>25%</th>
<th>median</th>
<th>75%</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>species richness (number of taxa)</td>
<td>15</td>
<td>7</td>
<td>1</td>
<td>10</td>
<td>15</td>
<td>19</td>
<td>41</td>
</tr>
<tr>
<td>water depth (m)</td>
<td>3.4</td>
<td>4.0</td>
<td>0</td>
<td>0.70</td>
<td>1.7</td>
<td>4.9</td>
<td>39</td>
</tr>
<tr>
<td>tidal amplitude (cm)</td>
<td>49</td>
<td>41</td>
<td>24</td>
<td>27</td>
<td>28</td>
<td>50</td>
<td>156</td>
</tr>
<tr>
<td>sedimentation rate (cm/y)</td>
<td>0.010</td>
<td>1.9</td>
<td>-8.2</td>
<td>-0.20</td>
<td>0.30</td>
<td>1.0</td>
<td>2.5</td>
</tr>
<tr>
<td>sediment sand content (%)</td>
<td>36</td>
<td>25</td>
<td>2.0</td>
<td>20</td>
<td>26</td>
<td>46</td>
<td>100</td>
</tr>
<tr>
<td>sediment clay content (%)</td>
<td>13</td>
<td>10</td>
<td>0.0</td>
<td>3.5</td>
<td>10</td>
<td>21</td>
<td>44</td>
</tr>
<tr>
<td>sediment dry matter content (%)</td>
<td>56</td>
<td>17</td>
<td>18</td>
<td>41</td>
<td>57</td>
<td>73</td>
<td>96</td>
</tr>
<tr>
<td>sediment organic matter content (%)</td>
<td>5.2</td>
<td>4.2</td>
<td>0.10</td>
<td>1.4</td>
<td>4.5</td>
<td>8.5</td>
<td>26</td>
</tr>
<tr>
<td>pH (-)</td>
<td>7.8</td>
<td>0.50</td>
<td>4.4</td>
<td>7.5</td>
<td>7.8</td>
<td>8.1</td>
<td>9.7</td>
</tr>
<tr>
<td>mixture toxic pressure (-)</td>
<td>0.13</td>
<td>0.077</td>
<td>0</td>
<td>0.075</td>
<td>0.14</td>
<td>0.17</td>
<td>0.42</td>
</tr>
</tbody>
</table>
Table 2. Three sets of fixed environmental conditions used to obtain f-SSDs from the S-SDMs.

<table>
<thead>
<tr>
<th>Variable (unit)</th>
<th>worst case conditions</th>
<th>median conditions</th>
<th>optimum conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>water depth (m)</td>
<td>39.0</td>
<td>1.7</td>
<td>0.0</td>
</tr>
<tr>
<td>sedimentation rate (cm/y)</td>
<td>-8.20</td>
<td>0.30</td>
<td>0.41</td>
</tr>
<tr>
<td>sediment sand content (%)</td>
<td>41</td>
<td>26</td>
<td>2</td>
</tr>
<tr>
<td>sediment organic matter content (%)</td>
<td>26</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>pH (-)</td>
<td>6.9</td>
<td>7.7</td>
<td>7.3</td>
</tr>
<tr>
<td>mixture toxic pressure (-)</td>
<td>0.23</td>
<td>0.14</td>
<td>0.11</td>
</tr>
<tr>
<td>Biesbosch area (-)</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>shipping (-)</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>